[0254] Still another aspect of the present invention relates to methods for generating non-human animals and stem cells having a functionally disrupted endogenous gene. In a preferred embodiment, the method comprises the steps of:

√[0255] (i) constructing a transgene construct including (a) a recombination region having at least a portion of an IBD gene, which recombination region directs recombination of the transgene with the gene, and (b) a marker sequence which provides a detectable signal for identifying the presence of the transgene in a cell;

√[0256] (ii) transfering the transgene into stem cells of a non-human animal;

[0257] (iii) selecting stem cells having a correctly targeted homologous recombination between the transgene and the gene;

[0258] (iv) transfering cells identified in step (iii) into a non-human blastocyst and implanting the resulting chimeric blastocyst into a non-human female; and

[0259] (v) collecting offspring harboring an endogenous gene allele having the correctly targeted recombination.

[0260] Yet another aspect of the invention provides a method for evaluating the potential of an agent to cause an IBD or to protect against development of an IBD by (i) contacting a transgenic animal of the present invention with a test agent, and (ii) ascertaining the presence, and more preferably the level, of onset or degree of severity of an inflammatory bowel disease or disorder, and comparing that with an untreated transgenic animal or transgenic animal preated with a control agent.

[0261] X. Exemplification

[0262] The following Table 1 teaches genes whose upregulation or down-regulation, as indicated by "\" and "\", respectively, has been found to be associated with UC and CD. The genes are grouped according to their general functionality, as follows,

[0263] I Chemokines+cytokines and growth factors

√ [0264] II Inflammatory mediators

[0265] III Cell cycle regulators/transcription factors

[0266] IV. Cancer Related

[0267] V HLA or immune function genes

[0268] VI Antimicrobial

[0269] VII ECM and remodelling

[0270] VIII Others: Carbohydrate metabolism, Fatty acid metabolism, Protein folding/modification/degradation

TABLE 1

		Microsatellite			
	UC	CD Acc No.	Gene Names	Chromosome	
I	†23.4	12.8 Y000 87	MDNCF/IL-8	4q13-q21	D4S392-D4S2947
Ī	†15.3	X54489	MGSA (GRO1)	4q21	D4S400-D4S1534
1	†7.9	M57731	MIP-2 (GRO2) .	4a21	D4S392-D4S2947
Į	18.9	14.1 M28130	IL8	4q13-q21	D4S392-D4S2947
I	16.8	†3.9 X57351	IP-10	11	pTEL-D11S1318
Į.	16	J04130	MIP-1 /SCYA4	17q21	D17S933-D17S800
I	13.4	X53800	MIP-2 (GRO3)	4q.2̀]	D4S400-D4S1534
ſ	†3.2	M69203	MIP-1 /SCYA2	17q21	D17S933-D17S800
ſ	14.6	X04500	pro-IL-1	2q14	D2S293-D2S121
I	13.5	X53296	IL-1RA	2q34	D2S293-D2S121
1	13.3	X04602	IL-6	7q21	D7S829-D7S673
. 1	13	J03756	Growth hormone 2 (GH2)	17q22-q24	D17S794-D17S795
ī	‡3.5	D16431	Hepatoma-derived growth factor (HDGF)	17q2–q24	D17S794-D17S795
Ī		14 M58286	TNF Receptor member 1A	12p13.2	D12S99-D12S358
ĬĬ	†35.5	S75256	Neutrophil lipocalin (HNL)	_	_
H	†10.4	X99133	Neutrophil gelatinase- associated lipocalin (NGAL)	9q34	D9S1821-D9S159
II	†8.7	X85781	Nitric oxide synthase (NOS2)		_
11	†5.1	X65965 M 2 2430	Mitochondrial superoxide	6q25.3	D6S442-D6S1581
II.	<b>†</b> 5.5	14.6 M44230)	dismutase (SOD2) Phospholipase A2, group IIA (PLA2G2A)	1p35	_
11	15.3	X51441	Serum amyloid A (SAA)	llp	_
П	13.9	J03474	Serum amyloid A (SAAI)	11p15.1	D11S921-D11S1369



TABLE 1-continued

				TABLE 1-Contin	100	
	UC	CD	Acc No.	Gene Names	Chromosome	Microsatellite Markers
٧	13	16	M84525	Complement factor D (DF)	_	pTEL-D19S413
v	13.9		M38690	CD9 antigen	12p13	D12S99-D12S358
V VI	†5 †20.4	† 40 :	M28590 8 M97925	MHC Dg Defensio 5	6 Spierp21	D8S552-D8S549
	•			(DEFA5)	Spite:-p±1	D65331-D65349
VI 	16.8	†7.°	7 U33317	Defensin 6 (DEFA6)	Spier-p21	D8S277-D8S550
VΠ	116.2	†3.	3 L23808	MMP-12 (Macrophage	11q22.2- q22.3	D11S1339- D11S1343
	• • •			elastase)	ŕ	
VU.	16.4		J05070	MMP-9 (Gelatinase B)	26q11.2- q13.1	D20S119-D20S197
VII	†4.7		X54925	MMP-1	11q22.3	D11S1339-
				(Interstitial collagenase)	D11S1343-	7
VΠ	14.2		X05232	MMP-3 (Stromelysin 1)	11q22.3	D11S1339-
VII	113.3	†3.8	8 L10343	Elastase specific	20q12-q13	D11S1343 D20S119-D20S197
				inhibitor (Elafin)		
VU	†11	†3.1	Z74616	COL1A2	2q37	D2S2158-D2S125
VII VII	† 7.3 † 6.9	13.6	X52022 5 M55998	COL6A3 COL1A1	2q37 17q21.3—	D2S2158-D2S125 D17S791-D17S794
	·	15.0		COLIAI	q22	D113191-D113194
VII VII	14.8 14.7		X06700 X15882	COL3A1	2q31	D2S2257-D2S115
VII	13.9		X05610	COL6A2 COL4A2	21q22.3 13q34	D13S2S5-qTEL
VII	13.7	†3.3	HG2157-	Mucin 4 (MUC4)	3q29	
VΠ	†3.1		HT2227 X52003	Trefoil factor 1	21q22.3	D21S1259-qTEL
VII		116	M22406	(TFF1) Intestinal mucin		
VII	†6.4	14.0	J03040	Osteonectin	5q31.3-	D5S436-D5S470
VII	14	†3.2	X17042	(SPARC) Proteoglycan 1	q32 10q22.1	D10S210-D10S537
VII	†3.9		D11428	(PRG1) Peripheral myelin	17p12-	D17S804-D17S799
				protein 22 (PMP22)	p11.2	
VII	†3.8		X02761	Fibronectin 1 (FN1)	2q34	D2S137-D2S164
∨ū	†3.7		M77349	Transforming	5q31	D5S393-D5S500
				growth factor beta-induced (TGF		
VII	13.2		D13666	f) Osteoblast	13	D13S267-D13S1253
				specific factor 2 (OSF-2)		
_v11	13.1		M10321	• •	12p13.3	D12S99-D12S358
VII	†3		L09190	Trichohyalin	1q21-q23	D1S439-D1S459
VII		†3.1	D88422	(THH) Cystalin A (CSTA)	3q21	_
VII			X58199	Adducin 2 (ADD2)	2p13p14	_
VΠ		†3.7	M86933	Amelogenia (AMELY)	Yp11.2	
ΛΠ		13.2	D45370	Adipose specific collagen-like 2 (APM2)	10	D10S1786-D10S541
VII		13.8	X73501	Cytokeratin 20		_
VII	14		U60061	Zygin 2	2	D2S367- D2S2230 :D2S177-
VЩ	V	$\odot$	AF006087	Actin-related	3	D2S119 D3S3591-D3S1283
VII	L	(1)x	D87460	complex Paraiemmin	10n13 3	5TEL_D106413
AIII	150.5	A,	D26416	Estemse D (ESD)	13q14.1-	pTEL-D19S413 D13S328-D13S168
VIII	14.7		M15656	Aldolase B	q14.2 9q21.3	D15S202-D15S157
			•	-	q22.2	

TABLE 1-continued

	UC	CD Acc No.	Gene Names	Chromosome	Microsateliite : Markers
VIII VIII		16.3 J04040 14.4 L31801	Giucagon (GCG) Monocarboxylate transporter 1	2q36-q37 1p13.2- p12	D2S156-D2S376 D1S418-D1S514
VIII	13	D10523	(MCT1) Oxoglutarate denydrogenase	7p14—p13	D7S521-D7S478
VIII	<b>ļ</b> 4	M12963	(OGDH) Alcohol dehydrogenase 1a	4q21–q23	- ·
vni	↓4.5	Y00339	(ADH1) Carbonic anhydrase II	8q22	D8\$275-D8\$273
VIII	14.9	\$3.1 L10955	(CA2) Carbonic anhydrase IV	17q23	_
VIII	<b>\$12.7</b>	\$3.1 L05144	(CA4) Phophoenolpyruvate carboxykinase	20q13.31	D20S183-D20S173
VIII	†3	U07158	1, soluble (PCK1) Syntaxin 4A	_	
VIII	†3 <del>-</del>	£) L27706	(STX4A) Chaperonin subunit 6A	7	D7S530-D7S509
VIII	<b>1</b> 7	‡3.1 J04093	(CCT6A) UDP-glycosyi- transferase 1	2	D2S2158-D2S125
VЩ	13.2	U20499	(UGT1) Sulfotransferase family 1A	16p11.2	_
VIII	13	M15182	(SULTTA3) -glucuronidase (GUSB)	7q21.11	_
^mi	14	U08854	UDP glucuronosyitrans- ferase precursor	4q13	D4S1619-D4S392
VIII	15	D87292	(UGT2B15) Thiosulfate sulfurtransferase (TST)	22	D228277-D228283
VIII	<b>‡13</b>	14 M22324	Aminopeptidase N/CD13 (ANPEP)	15q25-q26	D15S202-D15S157
VIII	Į12	‡7 M22960 -	Protective protein for b- galactosidase (PPGB)	20q13.1	D20S119-D20S197
VIII	†3.4	X90908	Fatty acid binding protein 6 (FABP6)	5q23-q35	_
VIII	٠.	†4.1 J02874	Fatty acid binding protein 4 (FABP4)	8q21	<u> </u>
VIII	13	M10050	Fatty acid binding protein 1 (FABP1)	11p15.5	D11S1318-D11S909
VIII	13	L24774	Mitochondrial d3, d2-CoA-isomerase .	_ D	•
VIII	14	D16294	Mitochondrial 3- oxoacyl-CoA thiolase (ACAA2)	18	1851118-10185474
VIII	14	M77144	3 b- hydroxysteroid dehydrogenase (HSD3B2))	1p13.1	D1S418-D1S514
VIII	<b>1</b> 5	D105.11	Mitochondrial acetoacetyl-CoA thiolase		_
νШ		Z80345	Acyl-Coenzyme A	12q22- qter	D12S366-D12S340
VIII	<b>1</b> 7	L11708	17 b-	16q24.1— q24.2	D16S515-D16S422